MODELING, SYNTHESIS AND *IN VITRO* SCREENING OF UNUSUAL AMINO ACIDS AND PEPTIDES AS PROTEASE INHIBITORS

<u>Armen Sargsyan¹</u>, Heghine Hakobyan¹, Zorayr Mardiyan¹, Silva Jamharyan¹, Ani Dadayan^{1,2}, Tatevik Sargsyan^{1,2}, Nelli Hovhannisyan^{1,2}

¹Scientific and Production Center "Armbiotechnology" NAS RA 14 Gyurjyan Str., Yerevan, 0056, Armenia ²Yerevan State University 1 A. Manoukyan Str. Yerevan, 0025, Armenia E-mail: armensargsyan@armbiotech.am Received 31 September 2022 Accepted 21 November 2022

ABSTRACT

Currently non-proteinogenic amino acids and synthetic peptides are widely used as building blocks in the drugs design. Many of these compounds are enzyme inhibitors or antimicrobials. Secreted Clostridium histolyticum collagenase is considered as a virulence factor and thus is an attractive target for fighting microbial infection. Trypsin is a target for the treatment of digestive disorders. This study was aimed to find new inhibitors of collagenase and trypsin. The interaction of non-proteinogenic amino acids and peptides with C. histolyticum collagenase and trypsin has been evaluated by Molecular Docking followed by the measurement of enzyme inhibition by selected compounds. According to the Docking analysis, N-tert-butoxycarbonylglycyl-(S)-2-amino-3-(4-((4-fluorophenyl)-ethynyl)-phenyl)- α -alanine has to demonstrate the most effective interaction with collagenase. Thus, the synthesis of this dipeptide was carried out. Measurement of enzymes activity revealed that both the dipeptide and the amino acid included in its structure inhibit collagenase and trypsin. The amino acid inhibited collagenase with $IC_{50} = 0.32$ mM and trypsin with $IC_{50} = 0.57$ mM. The dipeptide inhibited collagenase with $IC_{50} = 0.62$ mM and trypsin with $IC_{50} = 89$ uM.

Keywords: bacterial collagenase, molecular docking, inhibitor, peptide synthesis.

INTRODUCTION

Enantiomerically enriched non-proteinogenic amino acids are valuable compounds for drug design mainly due to their unique structure and two functional groups that are easily modified. Their introduction into peptides structure expands the search for essencial pharmacological agents. Many of these compounds appeared to be enzymes inhibitors or antimicrobial drugs. The majority of pharmacological targets (about 85 %) are proteins, mainly ion channels and enzymes [1]. The collagenases play a key role in remodeling and degradation of extracellular matrix. The imbalance of the activation and inhibition of collagenases is responsible in progression or inhibition of several diseases [2]. Inhibition of collagenase and elastase prevents the loss of skin elasticity induced by photoageing [3]. It was

established that inhibitors of clostridial collagenases act as antivirulence agents [4, 5].

Trypsin plays an important role in regulation of digestion process. Upregulation of trypsin activity causes pancreatitis and related diseases which are commonly treated by trypsin inhibitors. Different classes of collagenase and trypsin inhibitors were developed and tested, however inhibitors targeting these enzymes with high selectivity are still required.

Molecular docking approach is used to predict the interaction between non-protein amino acids and peptides with collagenase and trypsin. The inhibition of these enzymes by selected compounds was investigated by *in vitro* tests.

In this study the interaction of non-protein amino acids and peptides with collagenase and trypsin has been evaluated by Molecular Docking followed by selection of the most effective compounds. The ability of the prospective compounds to inhibit these enzymes has been investigated.

EXPERIMENTAL

Molecular docking

Structure of compounds were built by ChemBioOffice 2010 (ChemBio3D Ultra12.0). Ligand free energy was minimized using MM2 force field and truncated Newton-Raphson method. Crystallographic structure of collagenase G was taken from the Protein Data Bank of Research Collaboratory for Structural Bioinformatics (PDB ID: 2Y50). Water molecules were removed and polar hydrogens were added. Docking of ligand to enzyme was done by using AutoGrid 4, AutoDock Vina softwares [6]. The ligands were ranked using an energy-based scoring function and a grid-based protein-ligand interaction was used to speedup the score calculation. The most promising interaction models were chosen and hydrogen bounds lengths were measured for them.

Chemistry

The synthesis of dipeptide N-tert-butoxycarbonyl glycyl-(S)-2-amino-3-(4-((4-fluorophenyl)-ethynyl)phenyl)-α-alanine has been performed as follows (Fig. 1). At the first stage protected amino acid N-tertbutoxycarbonylglycine (N-Boc-Gly) was synthesized (3) by using glycine (Alfa Aesar CAS No.:56-40-6) (1) as a starting substance and di-tert-butylpyrocarbonate ([(CH₂),COCO]₂O) (Acros CAS No.:24424-99-5) (2) dissolved in i-propanol. Conversion of the N-Boc-Gly (3) to succinimide ester was done according to the scheme presented in Fig. 1. In this reaction N-hydroxysuccinimide (HOSu) (4) (MERCK CAS No.: 6066-82-6) and dicyclohexylcarbodiimide (DCC) (MERCK CAS No.: 538-75-0) were used as water splitting agents, and 1,4-dioxane (Acros CAS No.: 123-91-1) and methylene chloride (MERCK CAS No.: 75-09-2) were used as solvents. The reaction proceeded according to a previously developed methods [7, 8]. The stable N-Boc-Gly-N-oxysuccinimide ester (5) was obtained as a result of the reaction. At the next stage, the

Protected amino acid	Non-protein amino acid	Dipeptide	Chemical yield, %	Enantiomeric yield, %
OH 3	HO NH ₂	7 OH OH	70	95

Fig. 1. Scheme and yealds of synthesis of N-tert-butoxycarbonylglycyl -(S)- β -4-(4-fluorophenyl)-ethynyl)-phenyl)- α -alanine dipeptide.

condensation reaction of the activated ester of N-Boc-Gly with (S)- β -4-(4-fluorophenyl)-ethynyl)-phenyl)- α -alanine (6) (previously synthesized in the laboratory for the synthesis of amino acids and peptides) was carried out. This reaction proceeded in the presence of 0.5 N aqueous NaOH (Acros CAS No.:1310-73-2) in 1,4-dioxane at room temperature. As a result, N-Boc-Gly-(S)- β -4-(4-fluorophenyl)-ethynyl)-phenyl)- α -alanine (7) dipeptide was synthesized.

Materials

All reagents were purchased from corresponding firms and used without further purification. Thinlayer chromatography (TLC) was carried out on Merck aluminium foil backed sheets precoated with 0.2 mm Kielselgel 60 F254. Melting points (mp) were determined by "Elektrothermal". ¹H spectra were recorded on "Varian Mercury 30000 300 MHz spectrometer using TMS as internal standard. The NMR spectra were calibrated by solvent at 7.27 (CDCl₂), $3.31 \text{ (CD}_2\text{OD)}, 4.79 \text{ (D}_2\text{O)}, 2.50 \text{ ((CD}_2)_2\text{SO)}.$ The enantiomeric purity of the dipeptide was determined by HPLC ("Waters Alliance 2695 HPLC System") on a chiral phase of the Diaspher 110-Chirasel-E 16 m, 4.0 x 250 mm, mobile phase consisted of methanol:sodium phosphate monobasic buffer (20:80). Enantiomeric yield was proved by chiral HPLC analysis of the isolated amino acids.

Synthesis of N-Boc-Gly

0.247 g (0.0033 mol) of glycine was added to 0.35 mL of NaOH (0.5 M aqueous solution) in a flatbottomed flask, then 0.185 g (0.0022 mol) of NaHCO₃ (Acros CAS No.:144-55-8) dissolved in 5 mL of water was added. The mixture was stirred with a magnetic stirrer at room temperature until the glycine was dissolved. After that 0.792 g (0.0036 mol) of di-tertbutylpyrocarbonate dissolved in 3.3 mL of *i*-propanol ((CH₂)₂CHOH) (MERCK CAS No.: 67-63-0) was added. The mixture was stirred at room temperature for 2 hours, the reaction progress was monitored by TLC. The reaction was completed in two hours. Then the reaction mixture was diluted with water to 25 mL, the excessive reagent was extracted with ethyl acetate (MERCK CAS No.: 141-78-6) - 2 x 10 mL. 3 mL of 10 % aqueous solution of citric acid (MERCK CAS No.: 77-92-9) was added to the reaction mixture and

the formed N-Boc-Gly was reextracted by ethyl acetate (2 x 10 mL). After decantation, organic solvents were evaporated under vacuum at 50°C - 60°C. The target product was recrystallized from ethyl acetate - hexane (Alfa Aesar CAS No.:110-54-3) mixture (1:3), filtered and vacuum dried (50°C - 60°C). The yield of the reaction was 70 % (0.4 g). The authenticity and chemical purity of N-Boc-Gly white powdery crystals were checked and confirmed by the reference data [9].

Synthesis of N-Noc-Gly-succinimide ester (3)

0.291 g (0.0025 mol) of N-hydroxysuccinimide (2) dissolved in a mixture of 6 mL of 1,4 - dioxane and 3 mL of methylene chloride were added to 0.411 g (0.0023 mol) of N-Boc-Gly (1). 0.495 g (0.0024 mol) of DCC dissolved in 3 mL of 1,4 - dioxane was added to the reaction mixture, stirred for \sim 2 h at 0°C and 1 h at room temperature. The formed precipitate was filtered off, the solvent distilled off on a rotary evaporator and crystallized in a mixture of ethyl acetate: hexane (1:2). Yield of the end product was 75 % (0.469 g).

Synthesis of N-tert-butoxycarbonylglycyl-(S)-2-amino-3-(4-((4-fluorophenyl)-ethynyl)-phenyl)-α-alanine

 $0.538 \text{ g } (0.0019 \text{ mol}) \text{ of } (S)-\beta-4-(4-\text{fluorophenyl})$ ethynyl)-phenyl)-α-alanine in 3 mL of 1,4 - dioxane was placed in a flat - bottom flask and heated to 60°C. Then 6.75 mL of 0.5 M NaOH and 0.053 g (0.00063 mol) of NaHCO, were added to the reaction mixture. 0.463 g (0.0017 mol) of N-Boc-Gly-N-oxysuccinimide esther dissolved in 2 mL of 1.4 - dioxane was added 15 min later. The reaction mixture was stirred for 3 h at room temperature and kept at 5°C. The next day, 5 mL of ethyl acetate, 3 mL of 10 % citric acid solution and 0.2 g of NaCl (Acros CAS No.:7647-14-5) were added to the reaction mixture and stirred for 15 min. The formed organic layer was separated, dried by Na₂SO₄ (Acros CAS No.:7757-82-6) and the solvent was removed under vacuum at 50°C. The residue was recrystallized in ethyl acetate-hexane mixture (1:3). The reaction was monitored by thin-layer chromatography in the system of chloroform (MERCK CAS No.: 67-66-3): methanol (MERCK CAS No.: 67-56-1): ethyl acetate (3:2:1). The yield was 70 % (0.52 g). Found, %: C 65.36; H 5.93; N 5.97. C₂₄H₂₅FN₂O₅. Calculated, %: C 65.44; H 5.72; N 6.36. ¹H NMR (300 MHz, DMSO) $\delta = 1.42$ (9H, s, t-C₄H₀); 2.97 $(1H, dd, J_1 = 13.6, J_2 = 7.8)$ and 3.12 $(1H, dd, J_1 = 13.6, J_2)$ = 5.1, CH₂CH); 3.50 - 3.60 (1H,1H, dd J_1 = 16.6, J_2 = 5.8, NHCH₂); 4.54 (1H, td, J_1 = 7.8, J_2 = 5.1, CHNH); 6.44 (1H, t, J = 5.8, NHCH₂); 7.05 - 7.14 (2H, m, =CH); 7.20 - 7.24 (2H, m, =CH), 7.36 - 7.41 (2H, m, =CH); 7.47 - 7.54 (2H, m, =CH); 7.72 (1H, d, J = 7.8, NH); 10.4 (br, 1H, COOH).

Determination of collagenase activity

Collagenase activity was measured by the method based on determining free amino groups released as a result of substrate hydrolysis [10]. The reaction mixture contained 0.05 M 4-(2-hydroxyethyl)-1piperazineethanesulfonic acid (HEPES) buffer (MERCK CAS No.: 7365-45-9), pH 7.2, 10 mg mL⁻¹ gelatin (MERCK CAS No.: 9000-70-8) and 0.025 mg mL⁻¹ collagenase (Alfa Aesar CAS No.: 9001-12-1). The reaction proceeded at 37°C. The concentration of amino groups in the reaction mixture was determined by ortho-phthalaldehyde (OPA) reagent containing 0.2 M borate buffer, pH 9.7, 0.1667 mg mL⁻¹ OPA (Alfa Aesar CAS No.: 643-79-8) and 1.18 mM mercaptoethanol (Alfa Aesar CAS No.: 60-24-2). The aliquot (50 μL) was picked up every 30 min. The reaction was stopped by addition of 6 µL of 30 % trichloroacetic acid. OPA reagent (1.5 mL) and H₂O (1.5 mL) were added to aliquit and A₃₄₀ was recorded after 5 min incubation at 27°C.

Determination of trypsin activity

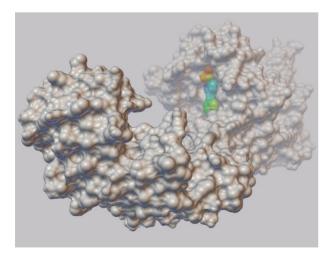
Trypsin activity was determined according to the method recommended by "Millipore" Corporation [11]. The reaction mixture contained 46 mM Tris·HCl buffer, pH

8.2 with 11.5 mM calcium chloride, 0.01 M $^{\alpha}$ N-p-Tosyl-L-Arg-OMexHCl (TAME) (MERCK CAS No.:1784-03-8). After incubation and temperature equilibration (3 - 4 minutes to achieve 25 $^{\circ}$ C), 12 ug mL $^{-1}$ trypsin (MERCK CAS No.: 9002-07-7) was added (0.1 mL of diluted enzyme). A₂₄₇ was recorded for 3 - 4 minutes. Δ A₂₄₇ was determined from initial linear portion of the curve. The reaction remained linear to an A₂₄₇ of about 0.320 [12].

RESULTS AND DISCUSSION

Docking of collagenase with non-protein amino acids synthesized earlier has been done. Inhibition of collagenase by the compounds that demonstrated the lowest ΔG (< -7.0 kcal mol⁻¹) was studied [13]. According to the results, (S)-2-amino-3-(4-((4-fluorophenyl)ethynyl)phenyl)- α -alanine (6) (ΔG - 7.5 kcal mol⁻¹) turned out to be the strongest inhibitor compared to the rest of studied compounds. The IC₅₀ for this compound was estimated to be 0.32 mM.

In this study, models of peptides containing **6** have been constructed and docking of these peptides with collagenase has been performed. According to the Docking data, dipeptide N-tert-butoxycarbonylglycyl-(S)-2-amino-3-(4-((4-fluorophenyl)ethynyl)phenyl)-α-alanine (**7**) demonstrated appropriate characteristics (ΔG -7.8 kcal mol⁻¹). Both compounds **6** and **7** bound collagenase symmetrically at the same site/pocket of catalytic subdomain (Fig. 2) [14]. The dipeptide (**7**) inhibited



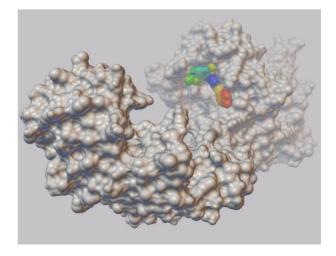


Fig. 2. Interaction of (S)-2-amino-3-(4-((4-fluorophenyl)-ethynyl)-phenyl)- α -alanine (a) and dipeptide N-tert-butoxycarbonylglycyl-(S)-2-amino-3-(4-((4-fluorophenyl)-ethynyl)-phenyl)- α -alanine (b) with colagenas according to molecular docking analysis.

collagenase with estimated $IC_{50} = 0.62$ mM.

The influence of **6** and **7** on the activity of trypsin has been also studied. Both compounds inhibited trypsin activity with estimated IC_{50} values of 89 uM for dipeptide (7) and 0.57 mM for amino acid (6). Thus, compounds (6 and 7) demonstrated the ability to inhibit both *C. histolyticum* collagenase (metalloprotease) and trypsin (serine protease).

CONCLUSIONS

New inhibitors of clostridial collagenase have been revealed in this study: (S)-2-amino-3-(4-((4-fluorophenyl)-ethynyl)-phenyl)- α -alanine (6) (IC₅₀ 0.32 mM) and dipeptide N-tert-butoxycarbonyl-glycyl-(S)-2-amino-3-(4-((4-fluorophenyl)-ethynyl)-phenyl)- α -alanine (7) (IC₅₀ = 0.62 mM).

According to the results, inhibition of collagenase by dipeptide was slightly decreased. On the other hand, the solubility of dipeptide (7) in H₂O was significantly higher compared to that of amino acid (6), which makes dipeptide more suitable for further application (data not shown). Both compounds inhibited trypsin activity. Estimated IC₅₀ value of 89 uM for dipeptide (7) suggests that this compound is a strong inhibitor of trypsin.

Acknowledgements

The work was supported by the Science Committee of RA in the frames of the research project No. 21T-2I235 and by ISTC in the frames of the research project No. A2705.

REFERENCES

- S.C. Bull, A.J. Doig, Properties of protein drug target classes, PLoS One, 10, 3, 2015, e0117955. doi:10.1371/journal.pone.0117955
- M. Raeeszadeh-Sarmazdeh, L.D. Do, B.G. Hritz, Metalloproteinases and Their Inhibitors: Potential for the Development of New Therapeutics, Cells, 9, 5, 2020, 1313. https://doi.org/10.3390/cells9051313
- K E. Leea, Sh. Bharadwaja, U. Yadavab, S.G. Kanga, Evaluation of caffeine as inhibitor against collagenase, elastase and tyrosinase using in silico and in vitro approach, J. Enzyme Inhib. Med. Chem., 34, 1, 2019, 927-936. https://doi.org/10.1080/14756 366.2019.1596904

- 4. J. Konstantinović, S. Yahiaoui, A. Alhayek, J. Haupenthal, E. Schönauer, A. Andreas, A.M. Kany, R. Müller, J. Koehnke, F.K. Berger, M. Bishoff, R.W. Hartmann, H. Brandstetter, A.K.H. Hirsch, N-Aryl-3-mercaptosuccinimides as Antivirulence Agents Targeting *Pseudomonas aeruginosa* Elastase and Clostridium Collagenases, J. Med. Chem., 63,15, 2020, 8359-8368.
- G. Nitulescu, G.M. Nitulescu, A. Zanifiresaku, D.P. Mihai, D. Gradinaru, Candidates for Repurposing as Anti-Virulence Agents Based on the Structural Profile Analysis of Microbial Collagenase Inhibitors, Pharmaceutics, 14, 1, 2022, 62, https://doi. org/10.3390/pharmaceutics14010062
- O. Trott, A. J. Olson, AutoDock Vina: Improving the speed and accuracy of docking with a new scoring function, efficient optimization, and multithreading, J. Comput. Chem., 31, 2, 2010, 455-461. doi: 10.1002/jcc.21334.
- 7. G. Anderson, J. Zimmerman, F. Callahan, The use of esters of n-hydroxysuccinimide in peptide synthesis, J. Am. Chem. Soc., 86, 9, 1964, 1839-1842.
- Yu. M. Dangyan, T.H. Sargsyan, S.M. Djamgaryan, E. A. Gyulumyan, H.A. Panosyan, A.S.Saghiyan. Synthesis of derivatives of di- and tripeptides with involvement of optically activenonprotein amino acids of α-allylglcine and β-(N-imidazolyl)alanine, Chemical journal of Armenia, 63, 2010, 95-100.
- 9. A.A. Gershkovich, V. K. Kibirev, Peptide synthesis, Reagents and methods, Kiev, Naukova dumka, 1987, 7-9 (In Russian).
- 10. W. Gade, J. Brown, Purification, characterization and possible function of alpha-N-acylamino acid hydrolase from bovine liver, Biochem. Bioph. Acta, 13, 1981, 86-93.
- 11. Worthington, Enzymes and related biochemical, Millipore Corporation, Bredford, 1997, pp 197-198.
- 12.N. Hovhannisyan, Sh. Harutyunyan, A. Hovhannisyan, A. Hambardzumyan, M. Chitchyan, M. Melkumyan, G. Oganezova, N. Avetisyan, The novel inhibitors of serine proteases, Amino Acids, 37, 3, 2009 531-536. doi: 10.1007/s00726-009-0257-4.
- 13. S. Parpart, Z.Z. Mardiyan, P. Ehlers, A. Petrosyan, A. F. Mkrtchyan, A. S. Saghyan, P. Langer, Synthesis of Optically Pure (S,E)-2-Amino-5-arylpent-4-enoic Acids by Heck Reactions of Nickel Complexes, Synlett, 29, 06, 2018 793-798, DOI: 10.1055/s-

0037-1609094

14. U. Eckhard, E. Schönauer, H. Brandstetter, Structural basis for activity regulation and substrate preference

of *clostridial* collagenases G, H, and T. J., Biol. Chem., 288, 28, 2013, 20184-94, doi: 10.1074/jbc. M112.448548.